

SEQUENCE LISTING

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<120> USE OF PROTEINS AND PEPTIDES CODED BY THE GENOME OF A NOVEL STRAIN OF
SARS-ASSOCIATED CORONAVIRUS

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<150> FR 0314152
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<170> PatentIn version 3.1

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 240 245 250

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tcttgctttg ttgcatgact agttgttgca gttgcctcaa ggggtgcatgc tcttggtggtt      60
cttgctgcaa gtttgatgag gatgactctg agccagttct caaggggtgtc aaattacatt      120
acacataaac gaacttatgg atttgtttat gagatttttt actccttggtat caattactgc      180
acagccagta aaaattgaca atgcttctcc tgcaagtact gttcatgcta cagcaacgat      240
accgctacaa gcctcactcc ctttcggatg gcttggtatt ggcgttgcat ttcttgctgt      300
ttttcagagc gctacaaaaa taattgctgct caataaaaga tggcagctag ccctttataa      360
gggcttccag ttcatttgca atttactgct gctatttggt accatctatt cacatctttt      420
gcttgctgct gcaggatgg aggcgcaatt tttgtacctc tatgccttga tatattttct      480
acaatgcata aacgcataga gaattattat gagatgttgg ctttggttga agtgcaaatac      540
caagaaccca ttactttt atg atg cca act act ttg ttt gct ggc aca cac      590
Met Met Pro Thr Thr Leu Phe Ala Gly Thr His
1 5 10
ata act atg act act gta tac cat ata aca gtg tca cag ata caa ttg      638
Ile Thr Met Thr Thr Val Tyr His Ile Thr Val Ser Gln Ile Gln Leu
15 20 25
tcg tta ctg aag gtg acg gca ttt caa cac caa aac tca aag aag act      686
Ser Leu Leu Lys Val Thr Ala Phe Gln His Gln Asn Ser Lys Lys Thr
30 35 40
acc aaa ttg gtg gtt att ctg agg ata ggc act cag gtg tta aag act      734
Thr Lys Leu Val Val Ile Leu Arg Ile Gly Thr Gln Val Leu Lys Thr
45 50 55
atg tcg ttg tac atg gct att tca ccg aag ttt act acc agc ttg agt      782
Met Ser Leu Tyr Met Ala Ile Ser Pro Lys Phe Thr Thr Ser Leu Ser
60 65 70 75
cta cac aaa tta cta cag aca ctg gta ttg aaa atg cta cat tct tca      830
Leu His Lys Leu Gln Thr Leu Val Leu Lys Met Leu His Ser Ser
80 85 90
tct tta aca agc ttg tta aag acc cac cga atg tgc aaa tac aca caa      878
Ser Leu Thr Ser Leu Leu Lys Thr His Arg Met Cys Lys Tyr Thr Gln
95 100 105
tcg acg gct ctt cag gag ttg cta atc cag caa tgg atc caa ttt atg      926
Ser Thr Ala Leu Gln Glu Leu Leu Ile Gln Gln Trp Ile Gln Phe Met
110 115 120
atg agc cga cga cga cta cta gcg tgc ctt tgt aag cac aag aaa gtg      974
Met Ser Arg Arg Arg Leu Leu Ala Cys Leu Cys Lys His Lys Lys Val
125 130 135
agt acg aac tta tgt act cat tcg ttt cgg aag aaa cag gta cgt      1019
Ser Thr Asn Leu Cys Thr His Ser Phe Arg Lys Lys Gln Val Arg
140 145 150
taatagttaa tagcgtaactt ctttttcttg ctttcgtggg attcttgcta gtcacactag      1079
ccatccttac tgcgctt      1096

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<210> 12
 <211> 154
 <212> PRT
 <213> CORONAVIRUS

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<400> 12
Met Met Pro Thr Thr Leu Phe Ala Gly Thr His Ile Thr Met Thr Thr
1 5 10 15
Val Tyr His Ile Thr Val Ser Gln Ile Gln Leu Ser Leu Lys Val
20 25 30
Thr Ala Phe Gln His Gln Asn Ser Lys Lys Thr Thr Lys Leu Val Val
35 40 45
Ile Leu Arg Ile Gly Thr Gln Val Leu Lys Thr Met Ser Leu Tyr Met
50 55 60
Ala Ile Ser Pro Lys Phe Thr Thr Ser Leu Ser Leu His Lys Leu Leu
65 70 75 80
Gln Thr Leu Val Leu Lys Met Leu His Ser Ser Ser Leu Thr Ser Leu
85 90 95
Leu Lys Thr His Arg Met Cys Lys Tyr Thr Gln Ser Thr Ala Leu Gln
100 105 110

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Glu Leu Leu Ile Gln Gln Trp Ile Gln Phe Met Met Ser Arg Arg Arg
 115 120 125
 Leu Leu Ala Cys Leu Cys Lys His Lys Lys Val Ser Thr Asn Leu Cys
 130 135 140
 Thr His Ser Phe Arg Lys Lys Gln Val Arg
 145 150

<210> 13
 <211> 332
 <212> DNA
 <213> CORONAVIRUS

<220>
 <221> CDS
 <222> (36)..(263)
 <223>

<400> 13
 tgcctttgta agcacaagaa agtgagtacg aactt atg tac tca ttc gtt tcg 53
 Met Tyr Ser Phe Val Ser
 1 5
 gaa gaa aca ggt acg tta ata gtt aat agc gta ctt ctt ttt ctt gct 101
 Glu Glu Thr Gly Thr Leu Ile Val Asn Ser Val Leu Leu Phe Leu Ala
 10 15 20
 ttc gtg gta ttc ttg cta gtc aca cta gcc atc ctt act gcg ctt cga 149
 Phe Val Val Phe Leu Leu Val Thr Leu Ala Ile Leu Thr Ala Leu Arg
 25 30 35
 ttg tgt gcg tac tgc tgc aat att gtt aac gtg agt tta gta aaa cca 197
 Leu Cys Ala Tyr Cys Cys Asn Ile Val Asn Val Ser Leu Val Lys Pro
 40 45 50
 acg gtt tac gtc tac tcg cgt gtt aaa aat ctg aac tct tct gaa gga 245
 Thr Val Tyr Val Tyr Ser Arg Val Lys Asn Leu Asn Ser Ser Glu Gly
 55 60 65 70
 gtt cct gat ctt ctg gtc taaacgaact aactattatt attattctgt 293
 Val Pro Asp Leu Leu Val
 75
 ttggaacttt aacattgctt atcatggcag acaacggta 332

<210> 14
 <211> 76
 <212> PRT
 <213> CORONAVIRUS

<400> 14
 Met Tyr Ser Phe Val Ser Glu Glu Thr Gly Thr Leu Ile Val Asn Ser
 1 5 10 15
 Val Leu Leu Phe Leu Ala Phe Val Val Phe Leu Leu Val Thr Leu Ala
 20 25 30
 Ile Leu Thr Ala Leu Arg Leu Cys Ala Tyr Cys Cys Asn Ile Val Asn
 35 40 45
 Val Ser Leu Val Lys Pro Thr Val Tyr Val Tyr Ser Arg Val Lys Asn
 50 55 60
 Leu Asn Ser Ser Glu Gly Val Pro Asp Leu Leu Val
 65 70 75

<210> 15
 <211> 332
 <212> DNA
 <213> CORONAVIRUS

<400> 15
 tgcctttgta agcacaagaa agtgagtacg aacttatgta ctcattcggtt tcggaagaaa 60

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caggtagcgtt aatagttaat agcgtacttc tttttcttgc tttcgtggta ttcttgctag 120
tcacactagc catccttact gcgcttcgat tgtgtgcgta ctgctgcaat attgttaacg 180
tgagtttagt aaaaccaacg gtttacgtct actcgcgtgt taaaaatctg aactcttctg 240
aaggagttcc tgatcttctg gtctaaacga actaactatt attattattc tgtttggaac 300
ttaacattg cttatcatgg cagacaacgg ta 332

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<210> 16
<211> 708
<212> DNA
<213> CORONAVIRUS

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<220>
<221> CDS
<222> (41)..(703)
<223>

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<400> 16
tattattatt attctgtttg gaactttaac attgcttatt atg gca gac aac ggt 55
Met Ala Asp Asn Gly
1 5
act att acc gtt gag gag ctt aaa caa ctc ctg gaa caa tgg aac cta 103
Thr Ile Thr Val Glu Glu Leu Lys Gln Leu Leu Glu Gln Trp Asn Leu
10 15 20
gta ata ggt ttc cta ttc cta gcc tgg att atg tta cta caa ttt gcc 151
Val Ile Gly Phe Leu Phe Leu Ala Trp Ile Met Leu Leu Gln Phe Ala
25 30 35
tat tct aat cgg aac agg ttt ttg tac ata ata aag ctt gtt ttc ctc 199
Tyr Ser Asn Arg Asn Arg Phe Leu Tyr Ile Ile Lys Leu Val Phe Leu
40 45 50
tgg ctc ttg tgg cca gta aca ctt gct tgt ttt gtg ctt gct gct gtc 247
Trp Leu Leu Trp Pro Val Thr Leu Ala Cys Phe Val Leu Ala Ala Val
55 60 65
tac aga att aat tgg gtg act ggc ggg att gcg att gca atg gct tgt 295
Tyr Arg Ile Asn Trp Val Thr Gly Gly Ile Ala Ile Ala Met Ala Cys
70 75 80 85
att gta ggc ttg atg tgg ctt agc tac ttc gtt gct tcc ttc agg ctg 343
Ile Val Gly Leu Met Trp Leu Ser Tyr Phe Val Ala Ser Phe Arg Leu
90 95 100
ttt gct cgt acc cgc tca atg tgg tca ttc aac cca gaa aca aac att 391
Phe Ala Arg Thr Arg Ser Met Trp Ser Phe Asn Pro Glu Thr Asn Ile
105 110 115
ctt ctc aat gtg cct ctc cgg ggg aca att gtg acc aga ccg ctc atg 439
Leu Leu Asn Val Pro Leu Arg Gly Thr Ile Val Thr Arg Pro Leu Met
120 125 130
gaa agt gaa ctt gtc att ggt gct gtg atc att cgt ggt cac ttg cga 487
Glu Ser Glu Leu Val Ile Gly Ala Val Ile Ile Arg Gly His Leu Arg
135 140 145
atg gcc gga cac tcc cta ggg cgc tgt gac att aag gac ctg cca aaa 535
Met Ala Gly His Ser Leu Gly Arg Cys Asp Ile Lys Asp Leu Pro Lys
150 155 160 165
gag atc act gtg gct aca tca cga acg ctt tct tat tac aaa tta gga 583
Glu Ile Thr Val Ala Thr Ser Arg Thr Leu Ser Tyr Tyr Lys Leu Gly
170 175 180
gcg tcg cag cgt gta ggc act gat tca ggt ttt gct gca tac aac cgc 631
Ala Ser Gln Arg Val Gly Thr Asp Ser Gly Phe Ala Ala Tyr Asn Arg
185 190 195
tac cgt att gga aac tat aaa tta aat aca gac cac gcc ggt agc aac 679
Tyr Arg Ile Gly Asn Tyr Lys Leu Asn Thr Asp His Ala Gly Ser Asn
200 205 210
gac aat att gct ttg cta gta cag taagt 708
Asp Asn Ile Ala Leu Leu Val Gln
215 220

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<210> 17
 <211> 221
 <212> PRT
 <213> CORONAVIRUS

<400> 17
 Met Ala Asp Asn Gly Thr Ile Thr Val Glu Glu Leu Lys Gln Leu Leu
 1 5 10 15
 Glu Gln Trp Asn Leu Val Ile Gly Phe Leu Phe Leu Ala Trp Ile Met
 20 25 30
 Leu Leu Gln Phe Ala Tyr Ser Asn Arg Asn Arg Phe Leu Tyr Ile Ile
 35 40 45
 Lys Leu Val Phe Leu Trp Leu Leu Trp Pro Val Thr Leu Ala Cys Phe
 50 55 60
 Val Leu Ala Ala Val Tyr Arg Ile Asn Trp Val Thr Gly Gly Ile Ala
 65 70 75 80
 Ile Ala Met Ala Cys Ile Val Gly Leu Met Trp Leu Ser Tyr Phe Val
 85 90 95
 Ala Ser Phe Arg Leu Phe Ala Arg Thr Arg Ser Met Trp Ser Phe Asn
 100 105 110
 Pro Glu Thr Asn Ile Leu Leu Asn Val Pro Leu Arg Gly Thr Ile Val
 115 120 125
 Thr Arg Pro Leu Met Glu Ser Glu Leu Val Ile Gly Ala Val Ile Ile
 130 135 140
 Arg Gly His Leu Arg Met Ala Gly His Ser Leu Gly Arg Cys Asp Ile
 145 150 155 160
 Lys Asp Leu Pro Lys Glu Ile Thr Val Ala Thr Ser Arg Thr Leu Ser
 165 170 175
 Tyr Tyr Lys Leu Gly Ala Ser Gln Arg Val Gly Thr Asp Ser Gly Phe
 180 185 190
 Ala Ala Tyr Asn Arg Tyr Arg Ile Gly Asn Tyr Lys Leu Asn Thr Asp
 195 200 205
 His Ala Gly Ser Asn Asp Asn Ile Ala Leu Leu Val Gln
 210 215 220

<210> 18
 <211> 769
 <212> DNA
 <213> CORONAVIRUS

<400> 18
 cctgatcttc tgggtctaaac gaactaacta ttattattat tctgtttgga actttaacat 60
 tgcttatcat ggcagacaac ggtactatta ccgttgagga gcttaaaca ctcctggaac 120
 aatggaacct agtaataggt ttcctattcc tagcctggat tatgttacta caatttgcct 180
 attctaattcg gaacagggtt ttgtacataa taaagcttgt tttcctctgg ctcttggtggc 240
 cagtaacact tgcttggttt gtgcttgctg ctgtctacag aattaattgg gtgactggcg 300
 ggattgcat tgcaatggct tgtattgtag gcttgatgtg gcttagctac ttcgttgctt 360
 ccttcaggct gtttgctcgt acccgctcaa tgtggtcatt caaccagaa acaaacattc 420
 ttctcaatgt gcctctccgg gggacaattg tgaccagacc gctcatggaa agtgaacttg 480
 tcattggtgc tgtgatcatt cgtggtcact tgcaatggc cggacactcc ctaggggcgt 540
 gtgacattaa ggacctgcca aaagagatca ctgtggctac atcacgaacg ctttcttatt 600
 acaaattagg agcgtcgcag cgtgtaggca ctgattcagg ttttgctgca tacaaccgct 660
 accgtattgg aaactataaa ttaaatacag accacgccgg tagcaacgac aatattgctt 720
 tgctagtaca gtaagtgaca acagatgttt catcttggtg acttcagg 769

<210> 19
 <211> 1231
 <212> DNA
 <213> CORONAVIRUS

<400> 19
 taccgtattg gaaactataa attaaataga gaccacgccg gtagcaacga caatattgct 60

ttgctagtag	acgtaagtgc	aacagatggt	tcattcttgt	gacttccagg	ttacaatagc	120
agagatat	attatcatta	tgaggacttt	caggattgct	atttggaatc	ttgacgttat	180
aataagttca	atagtgcagc	aattatttaa	gcctctaact	aagaagaatt	attcggagtt	240
agatgatgaa	gaacctatgg	agttagatta	tccataaaaac	gaacatgaaa	attattctct	300
tcctgacatt	gattgtattt	acatcttgcc	agctatatca	ctatcaggag	tgtgtagag	360
gtacgactgt	actactaaaa	gaaccttgcc	catcaggaa	atacgagggc	aattcaccat	420
ttcaccctct	tgctgacaat	aaatttgcac	taacttgcac	tagcacacac	tttgcttttg	480
cttggtgctga	cggtagctga	catacctatc	agctgcgtgc	aagatcagtt	tcacccaaaac	540
ttttcatcag	acaagaggag	gttcaacaag	agctctactc	gccacttttt	ctcattgttg	600
ctgctctagt	atttttaata	ctttgcttca	ccattaagag	aaagacagaa	tgaatgagct	660
cactttaatt	gacttctatt	tgtgcttttt	agcctttctg	ctattccttg	ttttaataat	720
gcttattata	ttttgggttt	cactcgaaat	ccaggatcta	gaagaacctt	gtacccaaagt	780
ctaaacgaac	atgaaacttc	tcattgtttt	gacttgtatt	tctctatgca	gttgcatatg	840
cactgtagta	cagcgctgtg	catctaataa	acctcatgtg	cttgaagatc	cttgtaaggt	900
acaacactag	gggtaatact	tatagcactg	cttggtcttg	tgctctagga	aagggttttac	960
cttttcatag	atggcacact	atggttcaaa	catgcacacc	taatgttact	atcaactgtc	1020
aagatccagc	tggtggtgcg	cttatagcta	ggtgttggtg	ccttcatgaa	ggtcaccaaa	1080
ctgctgcatt	tagagacgta	cttggtgttt	taaataaacg	aacaaattaa	aatgtctgat	1140
aatggacccc	aatcaaacca	acgtagtgc	ccccgcatta	catttggtgg	acccacagat	1200
tcaactgaca	ataaccagaa	tggaggacgc	a			1231

<210> 20
 <211> 1242
 <212> DNA
 <213> CORONAVIRUS

<400> 20						
gcatacaacc	gctaccgtat	tggaactat	aaattaaata	cagaccacgc	cggtagcaac	60
gacaatattg	ctttgctagt	acagtaagt	acaacagatg	tttcatcttg	ttgacttcca	120
ggttacaata	gcagagatat	tgattatcat	tatgaggact	ttcaggattg	ctatttgga	180
tcttgacgtt	ataataagtt	caatagtgcg	acagttattt	aagcctctaa	ctaagaagaa	240
ttattcggag	ttagatgatg	aagaacctat	ggagttagat	tatccataaa	acgaacatga	300
aaattattct	cttcctgaca	ttgattgtat	ttacatcttg	cgagctatat	cactatcagg	360
agtgtgttag	aggtacgact	gtactactaa	aagaaccttg	cccatcagga	acatacagg	420
gcaattcacc	atttcaccct	cttgctgaca	ataaatttgc	actaacttgc	actagcacac	480
actttgcttt	tgcttgctgt	gacggtagtc	gacataccta	tcagctgcgt	gcaagatcag	540
tttcacaaa	acttttcatc	agacaagagg	aggttcaaca	agagctctac	tcgccacttt	600
ttctcattgt	tgctgctcta	gtatttttaa	tactttgctt	caccattaag	agaaagacag	660
aatgaatgag	ctcactttta	ttgacttcta	tttgctgctt	ttagcctttc	tgctattcct	720
tgtttttaata	atgcttatta	tattttgggt	ttcactcgaa	atccaggatc	tagaagaacc	780
ttgtacaaa	gtctaaacga	acatgaaact	tctcattgtt	ttgacttgta	tttctctatg	840
cagttgcata	tgcaactgtg	tacagcgctg	tgcatcta	aaacctcatg	tgcttgaaga	900
tccttgtaag	gtacaacact	aggggttaata	cttatagcac	tgcttggctt	tgtgctctag	960
gaaaggtttt	accttttcat	agatggcaca	ctatggttca	aacatgcaca	cctaattgtta	1020
ctatcaactg	tcaagatcca	gctgggtggt	cgcttatagc	taggtgttgg	taccttcatg	1080
aaggtcacca	aactgctgca	tttagagacg	tacttgttgt	tttaaataaa	cgaacgaatt	1140
aaaatgtctg	ataatggacc	ccaatcaaac	caacgtagt	ccccccgc	tacatttggt	1200
ggacccacag	attcaactga	caataaccag	aatggaggac	gc		1242

<210> 21
 <211> 1231
 <212> DNA
 <213> CORONAVIRUS

<220>						
<221> CDS						
<222> (86)..(274)						
<223>						
<400> 21						
taccgtattg	gaaactataa	attaaataca	gaccacgccg	gtagcaacga	caatattgct	60


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ttgctagtagtac agtaagtgac aacag atg ttt cat ctt gtt gac ttc cag gtt      112
                               Met Phe His Leu Val Asp Phe Gln Val
                               1           5
aca ata gca gag ata ttg att atc att atg agg act ttc agg att gct      160
Thr Ile Ala Glu Ile Leu Ile Ile Ile Met Arg Thr Phe Arg Ile Ala
10           15           20           25
att tgg aat ctt gac gtt ata ata agt tca ata gtg aga caa tta ttt      208
Ile Trp Asn Leu Asp Val Ile Ile Ser Ser Ile Val Arg Gln Leu Phe
           30           35           40
aag cct cta act aag aag aat tat tgc gag tta gat gat gaa gaa cct      256
Lys Pro Leu Thr Lys Lys Asn Tyr Ser Glu Leu Asp Asp Glu Glu Pro
           45           50           55
atg gag tta gat tat cca taaaacgaac atgaaaatta ttctcttcct      304
Met Glu Leu Asp Tyr Pro
           60
gacattgatt gtatttacat cttgcgagct atatcactat caggagtggtg ttagaggtac      364
gactgtacta ctaaaagaac cttgcccac aggaacatac gagggcaatt caccatttca      424
ccctcttgct gacaataaat ttgcactaac ttgcactagc acacactttg cttttgcttg      484
tgctgacggg actcgacata cctatcagct gcgtgcaaga tcagtttcac caaaactttt      544
catcagacaa gaggagggtt aacaagagct ctactcgcca ctttttctca ttgttgctgc      604
tctagtattt ttaatacttt gcttcacat taagagaaaag acagaatgaa tgagctcact      664
ttaattgact tctatgttg ctttttagcc tttctgctat tccttgtttt aataatgctt      724
attatatttt ggttttcact cgaaatccag gatctagaag aaccttgtag caaagtctaa      784
acgaacatga aactttctcat tgttttgact tgtatttctc tatgcagttg catatgcact      844
gtagtacagc gctgtgcatc taataaacct catgtgcttg aagatccttg taaggtaaa      904
cactaggggt aatacttata gcactgcttg gctttgtgct ctaggaaagg ttttaccttt      964
tcatagatgg cacactatgg ttcaaacatg cacacctaag gttactatca actgtcaaga      1024
tccagctggg ggtgcgctta tagctagggtg ttggtacctt catgaagggt accaaactgc      1084
tgcatttaga gacgtacttg ttgttttaaa taaacgaaca aattaaaatg tctgataatg      1144
gaccccaatc aaaccaacgt agtgcccccc gcattacatt tgggtggacc acagattcaa      1204
ctgacaataa ccagaatgga ggacgca      1231

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<210> 22
 <211> 63
 <212> PRT
 <213> CORONAVIRUS

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<400> 22
Met Phe His Leu Val Asp Phe Gln Val Thr Ile Ala Glu Ile Leu Ile
1           5           10           15
Ile Ile Met Arg Thr Phe Arg Ile Ala Ile Trp Asn Leu Asp Val Ile
           20           25           30
Ile Ser Ser Ile Val Arg Gln Leu Phe Lys Pro Leu Thr Lys Lys Asn
           35           40           45
Tyr Ser Glu Leu Asp Asp Glu Glu Pro Met Glu Leu Asp Tyr Pro
           50           55           60

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<210> 23
 <211> 1231
 <212> DNA
 <213> CORONAVIRUS

<220>
 <221> CDS
 <222> (285)..(650)
 <223>

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<400> 23
taccgtattg gaaactataa attaaatata gaccacgccc gtagcaacga caatattgct      60
ttgctagtagtac agtaagtgac aacagatggt tcatcttggt gacttccagg ttacaatagc      120
agagatattg attatcatta tgaggacttt caggattgct atttggaatc ttgacgttat      180
aataagttca atagtggagac aattatttaa gcctctaact aagaagaatt attcggagtt      240

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agatgatgaa gaacctatgg agttagatta tccataaaac gaac atg aaa att att 296
                                   Met Lys Ile Ile
                                   1
ctc ttc ctg aca ttg att gta ttt aca tct tgc gag cta tat cac tat 344
Leu Phe Leu Thr Leu Ile Val Phe Thr Ser Cys Glu Leu Tyr His Tyr
5                               10                               15                               20
cag gag tgt gtt aga ggt acg act gta cta cta aaa gaa cct tgc cca 392
Gln Glu Cys Val Arg Gly Thr Thr Val Leu Leu Lys Glu Pro Cys Pro
                               25                               30                               35
tca gga aca tac gag ggc aat tca cca ttt cac cct ctt gct gac aat 440
Ser Gly Thr Tyr Glu Gly Asn Ser Pro Phe His Pro Leu Ala Asp Asn
                               40                               45                               50
aaa ttt gca cta act tgc act agc aca cac ttt gct ttt gct tgt gct 488
Lys Phe Ala Leu Thr Cys Thr Ser Thr His Phe Ala Phe Ala Cys Ala
                               55                               60                               65
gac ggt act cga cat acc tat cag ctg cgt gca aga tca gtt tca cca 536
Asp Gly Thr Arg His Thr Tyr Gln Leu Arg Ala Arg Ser Val Ser Pro
70                               75                               80
aaa ctt ttc atc aga caa gag gag gtt caa caa gag ctc tac tcg cca 584
Lys Leu Phe Ile Arg Gln Glu Glu Val Gln Gln Glu Leu Tyr Ser Pro
85                               90                               95                               100
ctt ttt ctc att gtt gct gct cta gta ttt tta ata ctt tgc ttc acc 632
Leu Phe Leu Ile Val Ala Ala Leu Val Phe Leu Ile Leu Cys Phe Thr
                               105                               110                               115
att aag aga aag aca gaa tgaatgagct cactttaatt gacttctatt 680
Ile Lys Arg Lys Thr Glu
120
tgtgcttttt agcctttctg ctattccttg ttttaataat gcttattata ttttggtttt 740
cactcgaaat ccaggatcta gaagaacctt gtaccaaagt ctaaacgaac atgaaacttc 800
tcattgtttt gacttggtatt tctctatgca gttgcatatg cactgtagta cagcgctgtg 860
catctaataa acctcatgtg cttgaagatc cttgtaaggt acaacactag gggtaatact 920
tatagcactg cttggctttg tgctctagga aagggttttac cttttcatag atggcacact 980
atgggttcaaa catgcacacc taatgttact atcaactgtc aagatccagc tgggtggtgcg 1040
cttatagcta ggtgttggtta ccttcatgaa ggtcacaaaa ctgctgcatt tagagacgta 1100
cttggtgttt taaataaacg aacaaattaa aatgtctgat aatggacccc aatcaaacca 1160
acgtagtgcc cccgcatta catttggtgg acccacagat tcaactgaca ataaccagaa 1220
tggaggacgc a 1231

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<210> 24
 <211> 122
 <212> PRT
 <213> CORONAVIRUS

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<400> 24
Met Lys Ile Ile Leu Phe Leu Thr Leu Ile Val Phe Thr Ser Cys Glu
1                               5                               10                               15
Leu Tyr His Tyr Gln Glu Cys Val Arg Gly Thr Thr Val Leu Leu Lys
20                               25                               30
Glu Pro Cys Pro Ser Gly Thr Tyr Glu Gly Asn Ser Pro Phe His Pro
35                               40                               45
Leu Ala Asp Asn Lys Phe Ala Leu Thr Cys Thr Ser Thr His Phe Ala
50                               55                               60
Phe Ala Cys Ala Asp Gly Thr Arg His Thr Tyr Gln Leu Arg Ala Arg
65                               70                               75                               80
Ser Val Ser Pro Lys Leu Phe Ile Arg Gln Glu Glu Val Gln Gln Glu
85                               90                               95
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<220>
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 <223>

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 ctgctctagt atttttaata ctttgcttca ccattaagag aaagacaga atg aat gag 658
 Met Asn Glu
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 ctc act tta att gac ttc tat ttg tgc ttt tta gcc ttt ctg cta ttc 706
 Leu Thr Leu Ile Asp Phe Tyr Leu Cys Phe Leu Ala Phe Leu Leu Phe
 5 10 15
 ctt gtt tta ata atg ctt att ata ttt tgg ttt tca ctc gaa atc cag 754
 Leu Val Leu Ile Met Leu Ile Ile Phe Trp Phe Ser Leu Glu Ile Gln
 20 25 30 35
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 Asp Leu Glu Glu Pro Cys Thr Lys Val
 40
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 <212> PRT
 <213> CORONAVIRUS

<400> 26
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 Glu Ile Gln Asp Leu Glu Glu Pro Cys Thr Lys Val
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 <212> DNA
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<220>
 <221> CDS

<222> (791)..(907)

<223>

<400> 27

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Ser Cys Ile Cys Thr Val Val Gln Arg Cys Ala Ser Asn Lys Pro His						
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Val Leu Glu Asp Pro Cys Lys Val Gln His						
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<212> PRT

<213> CORONAVIRUS

<400> 28

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<223>

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Met Cys Leu Lys Ile Leu
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Ala	Leu	Gly	Lys	Val	Leu	Pro	Phe	His	Arg	Trp	His	Thr	Met	Val	Gln	
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<212> PRT
<213> CORONAVIRUS

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35 40 45
Gln Asp Pro Ala Gly Gly Ala Leu Ile Ala Arg Cys Trp Tyr Leu His
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<210> 31
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<210> 32
 <211> 297
 <212> DNA
 <213> CORONAVIRUS

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aacttagatt	ccctcgaggg	cagggcggtc	caatcaacac	caatagtggg	ccagatgacc	240
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 <211> 98
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 <213> CORONAVIRUS

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Gln Gly Gln Asn Ser Ala Asp Pro Lys Val Tyr Pro Ile Ile Leu Arg	
35 40 45	

Leu Gly Ser Gln Leu Ser Leu Ser Met Ala Arg Arg Asn Leu Asp Ser
 50 55 60
 Leu Glu Ala Arg Ala Phe Gln Ser Thr Pro Ile Val Val Gln Met Thr
 65 70 75 80
 Lys Leu Ala Thr Thr Glu Glu Leu Pro Asp Glu Phe Val Val Val Thr
 85 90 95
 Ala Lys

<210> 34
 <211> 213
 <212> DNA
 <213> CORONAVIRUS

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 caagaaattc aactcctggc agcagtaggg gaaattctcc tgctcgaatg gctagcggag 180
 gtgggtgaaac tgccctcgcg ctattgctgc tag 213

<210> 35
 <211> 70
 <212> PRT
 <213> CORONAVIRUS

<400> 35
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 20 25 30
 Pro His His Val Val Ala Val Ile Gln Glu Ile Gln Leu Leu Ala Ala
 35 40 45
 Val Gly Glu Ile Leu Leu Leu Glu Trp Leu Ala Glu Val Val Lys Leu
 50 55 60
 Pro Ser Arg Tyr Cys Cys
 65 70

<210> 36
 <211> 1377
 <212> DNA
 <213> CORONAVIRUS

<220>
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 Met Ser Asp Asn Gly Pro Gln Ser Asn Gln Arg Ser Ala Pro
 1 5 10
 cgc att aca ttt ggt gga ccc aca gat tca act gac aat aac cag aat 156
 Arg Ile Thr Phe Gly Gly Pro Thr Asp Ser Thr Asp Asn Asn Gln Asn
 15 20 25 30
 gga gga cgc aat ggg gca agg cca aaa cag cgc cga ccc caa ggt tta 204
 Gly Gly Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu
 35 40 45
 ccc aat aat act gcg tct tgg ttc aca gct ctc act cag cat ggc aag 252
 Pro Asn Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys
 50 55 60

gag gaa ctt aga ttc cct cga ggc cag ggt cca atc aac acc aat	300
Glu Glu Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn	
65 70 75	
agt ggt cca gat gac caa att ggc tac tac cga aga gct acc cga cga	348
Ser Gly Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg	
80 85 90	
ggt cgt ggt ggt gac ggc aaa atg aaa gag ctc agc ccc aga tgg tac	396
Val Arg Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr	
95 100 105 110	
ttc tat tac cta gga act ggc cca gaa gct tca ctt ccc tac ggc gct	444
Phe Tyr Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala	
115 120 125	
aac aaa gaa ggc atc gta tgg gtt gca act gag gga gcc ttg aat aca	492
Asn Lys Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr	
130 135 140	
ccc aaa gac cac att ggc acc cgc aat cct aat aac aat gct gcc acc	540
Pro Lys Asp His Ile Gly Thr Arg Asn Pro Asn Asn Asn Ala Ala Thr	
145 150 155	
gtg cta caa ctt cct caa gga aca aca ttg cca aaa ggc ttc tac gca	588
Val Leu Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala	
160 165 170	
gag gga agc aga ggc ggc agt caa gcc tct tct cgc tcc tca tca cgt	636
Glu Gly Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg	
175 180 185 190	
agt cgc ggt aat tca aga aat tca act cct ggc agc agt agg gga aat	684
Ser Arg Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn	
195 200 205	
tct cct gct cga atg gct agc gga ggt ggt gaa act gcc ctc gcg cta	732
Ser Pro Ala Arg Met Ala Ser Gly Gly Gly Glu Thr Ala Leu Ala Leu	
210 215 220	
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Leu Leu Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys	
225 230 235	
ggc caa caa caa caa ggc caa act gtc act aag aaa tct gct gct gag	828
Gly Gln Gln Gln Gln Gly Thr Val Thr Lys Lys Ser Ala Ala Glu	
240 245 250	
gca tct aaa aag cct cgc caa aaa cgt act gcc aca aaa cag tac aac	876
Ala Ser Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn	
255 260 265 270	
gtc act caa gca ttt ggg aga cgt ggt cca gaa caa acc caa gga aat	924
Val Thr Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn	
275 280 285	
ttc ggg gac caa gac cta atc aga caa gga act gat tac aaa cat tgg	972
Phe Gly Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp	
290 295 300	
ccg caa att gca caa ttt gct cca agt gcc tct gca ttc ttt gga atg	1020
Pro Gln Ile Ala Gln Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met	
305 310 315	
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Ser Arg Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr	
320 325 330	
cat gga gcc att aaa ttg gat gac aaa gat cca caa ttc aaa gac aac	1116
His Gly Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn	
335 340 345 350	
gtc ata ctg ctg aac aag cac att gac gca tac aaa aca ttc cca cca	1164
Val Ile Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro	
355 360 365	
aca gag cct aaa aag gac aaa aag aaa aag act gat gaa gct cag cct	1212
Thr Glu Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro	
370 375 380	

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gct gac atg gat gat ttc tcc aga caa ctt caa aat tcc atg agt gga      1308
Ala Asp Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly
      400                      405                      410
gct tct gct gat tca act cag gca taa acatcatga tgaccacaca      1355
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<210> 37
<211> 422
<212> PRT
<213> CORONAVIRUS

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      20                      25                      30
Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn
      35                      40                      45
Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu
      50                      55                      60
Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly
65                      70                      75                      80
Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Val Arg
      85                      90                      95
Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr Phe Tyr
      100                      105                      110
Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala Asn Lys
      115                      120                      125
Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr Pro Lys
      130                      135                      140
Asp His Ile Gly Thr Arg Asn Pro Asn Asn Asn Ala Ala Thr Val Leu
145                      150                      155                      160
Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly
      165                      170                      175
Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg Ser Arg
      180                      185                      190
Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn Ser Pro
      195                      200                      205
Ala Arg Met Ala Ser Gly Gly Glu Thr Ala Leu Ala Leu Leu Leu
      210                      215                      220
Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln
225                      230                      235                      240
Gln Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser
      245                      250                      255
Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr
      260                      265                      270
Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly
      275                      280                      285
Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln
290                      295                      300
Ile Ala Gln Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg
305                      310                      315                      320
Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly
      325                      330                      335
Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile
      340                      345                      350

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Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu
 355 360 365
 Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro
 370 375 380
 Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp
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 Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser
 405 410 415
 Ala Asp Ser Thr Gln Ala
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<210> 38
 <211> 1377
 <212> DNA
 <213> CORONAVIRUS

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<210> 39
 <211> 204
 <212> DNA
 <213> CORONAVIRUS

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<210> 40
 <211> 809
 <212> DNA
 <213> CORONAVIRUS

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 gcctctgcat tctttggaat gtcacgcatt ggcatggaag tcacaccttc gggaacatgg 180
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<210> 41
 <211> 448
 <212> DNA
 <213> CORONAVIRUS

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<210> 42
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 <212> DNA
 <213> CORONAVIRUS

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 <211> 2018
 <212> DNA
 <213> CORONAVIRUS

<400> 43

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 <213> CORONAVIRUS

<400> 44

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<212> DNA

<213> CORONAVIRUS

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<210> 46

<211> 1995

<212> DNA

<213> CORONAVIRUS

<400> 46

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 <211> 1884
 <212> DNA
 <213> CORONAVIRUS

<400> 47						
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 <211> 2020
 <212> DNA

<213> CORONAVIRUS

<400> 48

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<210> 49

<211> 2040

<212> DNA

<213> CORONAVIRUS

<400> 49

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 <211> 2012
 <212> DNA
 <213> CORONAVIRUS

<400> 50						
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<210> 51
 <211> 1877
 <212> DNA

<213> CORONAVIRUS

<400> 51

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<210> 52

<211> 2051

<212> DNA

<213> CORONAVIRUS

<400> 52

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<210> 53

<211> 2075

<212> DNA

<213> CORONAVIRUS

<400> 53

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<210> 54

<211> 1891

<212> DNA

<213> CORONAVIRUS

<400> 54

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<211> 32

<212> DNA

<213> artificial sequence

<220>

<223> N sens primer

<400> 55

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<211> 32

<212> DNA

<213> artificial sequence

<220>

<223> N antisens primer

<400> 56

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<211> 31

<212> DNA

<213> artificial sequence
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 <223> Sc sens primer
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 <211> 30
 <212> DNA
 <213> artificial sequence
 <220>
 <223> SL sens primer
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 <211> 33
 <212> DNA
 <213> Sc and SL antisens primer
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 <213> Antisens set 2 (28774-28759) primer
 <400> 61
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 <210> 62
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35 40 45
Gly Thr Cys Gly Leu Val Glu Leu Glu Lys Gly Val Leu Pro Gln Leu
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Glu Gln Pro Tyr Val Phe Ile Lys Arg Ser Asp Ala Leu Ser Thr Asn
65 70 75 80
His Gly His Lys Val Val Glu Leu Val Ala Glu Met Asp Gly Ile Gln
85 90 95
Tyr Gly Arg Ser Gly Ile Thr Leu Gly Val Leu Val Pro His Val Gly
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Trp	Asn	Thr	Lys	His	Gly	Ser	Gly	Ala	Leu	Arg	Glu	Leu	Thr	Arg	Glu
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Phe	Thr	Glu	Arg	Ser	Asp	Lys	Ser	Tyr	Glu	His	Gln	Thr	Pro	Phe	Glu
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Ile	Lys	Ser	Ala	Lys	Lys	Phe	Asp	Thr	Phe	Lys	Gly	Glu	Cys	Pro	Lys
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Pro	Cys	Pro	Ala	Cys	Gln	Asp	Pro	Glu	Ile	Gly	Pro	Glu	His	Ser	Val
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Gly	Arg	Thr	Arg	Cys	Phe	Gly	Gly	Cys	Val	Phe	Ala	Tyr	Val	Gly	Cys
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Tyr	Asn	Lys	Arg	Ala	Tyr	Trp	Val	Pro	Arg	Ala	Ser	Ala	Asp	Ile	Gly
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Asp 650	Cys 655	Val 660	Lys 665	Cys 670	Phe 675	Ile 680	Asp 685	Val 690	Val 695	Asn 700	Lys 705	Ala 710	Leu 715	Glu 720	Met 725
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Ile 680	Arg 685	Gly 690	Lys 695	Glu 700	Gln 705	Leu 710	Gln 715	Leu 720	Leu 725	Met 730	Pro 735	Leu 740	Lys 745	Ala 750	Pro 755
Lys 685	Glu 690	Val 695	Thr 700	Phe 705	Leu 710	Glu 715	Gly 720	Asp 725	Ser 730	His 735	Asp 740	Thr 745	Val 750	Leu 755	Thr 760
Ser 690	Glu 695	Glu 700	Val 705	Val 710	Leu 715	Lys 720	Asn 725	Gly 730	Glu 735	Leu 740	Glu 745	Ala 750	Leu 755	Glu 760	Thr 765
Pro 695	Val 700	Asp 705	Ser 710	Phe 715	Thr 720	Asn 725	Gly 730	Ala 735	Ile 740	Val 745	Gly 750	Thr 755	Pro 760	Val 765	Cys 770
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Ala 705	Leu 710	Ser 715	Pro 720	Gly 725	Leu 730	Leu 735	Ala 740	Thr 745	Asn 750	Asn 755	Val 760	Phe 765	Arg 770	Leu 775	Lys 780
Gly 710	Gly 715	Ala 720	Pro 725	Ile 730	Lys 735	Gly 740	Val 745	Thr 750	Phe 755	Gly 760	Glu 765	Asp 770	Thr 775	Val 780	Trp 785
Glu 715	Val 720	Gln 725	Gly 730	Tyr 735	Lys 740	Asn 745	Val 750	Arg 755	Ile 760	Thr 765	Phe 770	Glu 775	Leu 780	Asp 785	Glu 790
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Val 730	Lys 735	Thr 740	Leu 745	Gln 750	Pro 755	Val 760	Ser 765	Asp 770	Leu 775	Leu 780	Thr 785	Asn 790	Met 795	Gly 800	Ile 805
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Asp 745	Glu 750	Glu 755	Glu 760	Glu 765	Asp 770	Asp 775	Ala 780	Glu 785	Cys 790	Glu 795	Glu 800	Glu 805	Glu 810	Ile 815	Asp 820
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1160						1165					1170			
Pro	Arg	Val	Glu	Ala	Pro	Lys	Gln	Glu	Glu	Pro	Pro	Asn	Thr	Glu
1175						1180					1185			
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1190						1195					1200			
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Asp	Ile	Asn	Gly	Lys	Leu	Tyr	His	Asp	Ser	Gln	Asn	Met	Leu	Arg
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Ser	Lys	Lys	Ala	Gly	Gly	Thr	Thr	Glu	Met	Leu	Ser	Arg	Ala	Leu
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1340						1345					1350			
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1355						1360					1365			
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1385						1390					1395			
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2015						2020					2025			

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Tyr	Val	Lys	Ser	Pro	Lys	Phe	Ser	Lys	Leu	Phe	Thr	Ile	Ala	Met
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2225						2230					2235			
Tyr	Cys	Asn	Gly	Val	Arg	Glu	Leu	Tyr	Leu	Asn	Ser	Ser	Asn	Val
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Ile	Gln	Val	Thr	Ile	Ser	Ser	Tyr	Lys	Leu	Asp	Leu	Thr	Ile	Leu
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Gly	Leu	Ala	Ala	Glu	Trp	Val	Leu	Ala	Tyr	Met	Leu	Phe	Thr	Lys
2300						2305					2310			
Phe	Phe	Tyr	Leu	Leu	Gly	Leu	Ser	Ala	Ile	Met	Gln	Val	Phe	Phe
2315						2320					2325			
Gly	Tyr	Phe	Ala	Ser	His	Phe	Ile	Ser	Asn	Ser	Trp	Leu	Met	Trp
2330						2335					2340			
Phe	Ile	Ile	Ser	Ile	Val	Gln	Met	Ala	Pro	Val	Ser	Ala	Met	Val
2345						2350					2355			
Arg	Met	Tyr	Ile	Phe	Phe	Ala	Ser	Phe	Tyr	Tyr	Ile	Trp	Lys	Ser
2360						2365					2370			
Tyr	Val	His	Ile	Met	Asp	Gly	Cys	Thr	Ser	Ser	Thr	Cys	Met	Met
2375						2380					2385			
Cys	Tyr	Lys	Arg	Asn	Arg	Ala	Thr	Arg	Val	Glu	Cys	Thr	Thr	Ile
2390						2395					2400			
Val	Asn	Gly	Met	Lys	Arg	Ser	Phe	Tyr	Val	Tyr	Ala	Asn	Gly	Gly
2405						2410					2415			
Arg	Gly	Phe	Cys	Lys	Thr	His	Asn	Trp	Asn	Cys	Leu	Asn	Cys	Asp
2420						2425					2430			
Thr	Phe	Cys	Thr	Gly	Ser	Thr	Phe	Ile	Ser	Asp	Glu	Val	Ala	Arg
2435						2440					2445			
Asp	Leu	Ser	Leu	Gln	Phe	Lys	Arg	Pro	Ile	Asn	Pro	Thr	Asp	Gln
2450						2455					2460			
Ser	Ser	Tyr	Ile	Val	Asp	Ser	Val	Ala	Val	Lys	Asn	Gly	Ala	Leu
2465						2470					2475			
His	Leu	Tyr	Phe	Asp	Lys	Ala	Gly	Gln	Lys	Thr	Tyr	Glu	Arg	His
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Pro	Leu	Ser	His	Phe	Val	Asn	Leu	Asp	Asn	Leu	Arg	Ala	Asn	Asn	
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Thr	Lys	Gly	Ser	Leu	Pro	Ile	Asn	Val	Ile	Val	Phe	Asp	Gly	Lys	
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Ser	Lys	Cys	Asp	Glu	Ser	Ala	Ser	Lys	Ser	Ala	Ser	Val	Tyr	Tyr	
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Ser	Gln	Leu	Met	Cys	Gln	Pro	Ile	Leu	Leu	Leu	Asp	Gln	Ala	Leu	
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Val	Ser	Asp	Val	Gly	Asp	Ser	Thr	Glu	Val	Ser	Val	Lys	Met	Phe	
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Asp	Ala	Tyr	Val	Asp	Thr	Phe	Ser	Ala	Thr	Phe	Ser	Val	Pro	Met	
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Glu	Lys	Leu	Lys	Ala	Leu	Val	Ala	Thr	Ala	His	Ser	Glu	Leu	Ala	
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Lys	Gly	Val	Ala	Leu	Asp	Gly	Val	Leu	Ser	Thr	Phe	Val	Ser	Ala	
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Ala	Arg	Gln	Gly	Val	Val	Asp	Thr	Asp	Val	Asp	Thr	Lys	Asp	Val	
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Ile	Glu	Cys	Leu	Lys	Leu	Ser	His	His	Ser	Asp	Leu	Glu	Val	Thr	
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Gly	Asp	Ser	Cys	Asn	Asn	Phe	Met	Leu	Thr	Tyr	Asn	Lys	Val	Glu	
	2645					2650					2655				
Asn	Met	Thr	Pro	Arg	Asp	Leu	Gly	Ala	Cys	Ile	Asp	Cys	Asn	Ala	
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Arg	His	Ile	Asn	Ala	Gln	Val	Ala	Lys	Ser	His	Asn	Val	Ser	Leu	
	2675					2680					2685				
Ile	Trp	Asn	Val	Lys	Asp	Tyr	Met	Ser	Leu	Ser	Glu	Gln	Leu	Arg	
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Lys	Gln	Ile	Arg	Ser	Ala	Ala	Lys	Lys	Asn	Asn	Ile	Pro	Phe	Arg	
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Leu	Thr	Cys	Ala	Thr	Thr	Arg	Gln	Val	Val	Asn	Val	Ile	Thr	Thr	
	2720					2725					2730				
Lys	Ile	Ser	Leu	Lys	Gly	Gly	Lys	Ile	Val	Ser	Thr	Cys	Phe	Lys	
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Leu	Met	Leu	Lys	Ala	Thr	Leu	Leu	Cys	Val	Leu	Ala	Ala	Leu	Val	
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Cys	Tyr	Ile	Val	Met	Pro	Val	His	Thr	Leu	Ser	Ile	His	Asp	Gly	
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Tyr	Thr	Asn	Glu	Ile	Ile	Gly	Tyr	Lys	Ala	Ile	Gln	Asp	Gly	Val	
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Thr	Arg	Asp	Ile	Ile	Ser	Thr	Asp	Asp	Cys	Phe	Ala	Asn	Lys	His	
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Ala	Gly	Phe	Asp	Ala	Trp	Phe	Ser	Gln	Arg	Gly	Gly	Ser	Tyr	Lys	
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Asn	Asp	Lys	Ser	Cys	Pro	Val	Val	Ala	Ala	Ile	Ile	Thr	Arg	Glu	
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Ile	Gly	Phe	Ile	Val	Pro	Gly	Leu	Pro	Gly	Thr	Val	Leu	Arg	Ala	
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Ile	Asn	Gly	Asp	Phe	Leu	His	Phe	Leu	Pro	Arg	Val	Phe	Ser	Ala	
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Val	Gly	Asn	Ile	Cys	Tyr	Thr	Pro	Ser	Lys	Leu	Ile	Glu	Tyr	Ser	
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Asp	Phe	Ala	Thr	Ser	Ala	Cys	Val	Leu	Ala	Ala	Glu	Cys	Thr	Ile	
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Phe	Lys	Asp	Ala	Met	Gly	Lys	Pro	Val	Pro	Tyr	Cys	Tyr	Asp	Thr	
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Asn	Leu	Leu	Glu	Gly	Ser	Ile	Ser	Tyr	Ser	Glu	Leu	Arg	Pro	Asp	
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Thr	Arg	Tyr	Val	Leu	Met	Asp	Gly	Ser	Ile	Ile	Gln	Phe	Pro	Asn	
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Thr	Tyr	Leu	Glu	Gly	Ser	Val	Arg	Val	Val	Thr	Thr	Phe	Asp	Ala	
	2945					2950					2955				

Glu Tyr Cys Arg His Gly Thr Cys Glu Arg Ser Glu Val Gly Ile	2960	2965	2970
Cys Leu Ser Thr Ser Gly Arg Trp Val Leu Asn Asn Glu His Tyr	2975	2980	2985
Arg Ala Leu Ser Gly Val Phe Cys Gly Val Asp Ala Met Asn Leu	2990	2995	3000
Ile Ala Asn Ile Phe Thr Pro Leu Val Gln Pro Val Gly Ala Leu	3005	3010	3015
Asp Val Ser Ala Ser Val Val Ala Gly Gly Ile Ile Ala Ile Leu	3020	3025	3030
Val Thr Cys Ala Ala Tyr Tyr Phe Met Lys Phe Arg Arg Val Phe	3035	3040	3045
Gly Glu Tyr Asn His Val Val Ala Ala Asn Ala Leu Leu Phe Leu	3050	3055	3060
Met Ser Phe Thr Ile Leu Cys Leu Val Pro Ala Tyr Ser Phe Leu	3065	3070	3075
Pro Gly Val Tyr Ser Val Phe Tyr Leu Tyr Leu Thr Phe Tyr Phe	3080	3085	3090
Thr Asn Asp Val Ser Phe Leu Ala His Leu Gln Trp Phe Ala Met	3095	3100	3105
Phe Ser Pro Ile Val Pro Phe Trp Ile Thr Ala Ile Tyr Val Phe	3110	3115	3120
Cys Ile Ser Leu Lys His Cys His Trp Phe Phe Asn Asn Tyr Leu	3125	3130	3135
Arg Lys Arg Val Met Phe Asn Gly Val Thr Phe Ser Thr Phe Glu	3140	3145	3150
Glu Ala Ala Leu Cys Thr Phe Leu Leu Asn Lys Glu Met Tyr Leu	3155	3160	3165
Lys Leu Arg Ser Glu Thr Leu Leu Pro Leu Thr Gln Tyr Asn Arg	3170	3175	3180
Tyr Leu Ala Leu Tyr Asn Lys Tyr Lys Tyr Phe Ser Gly Ala Leu	3185	3190	3195
Asp Thr Thr Ser Tyr Arg Glu Ala Ala Cys Cys His Leu Ala Lys	3200	3205	3210
Ala Leu Asn Asp Phe Ser Asn Ser Gly Ala Asp Val Leu Tyr Gln	3215	3220	3225
Pro Pro Gln Thr Ser Ile Thr Ser Ala Val Leu Gln Ser Gly Phe	3230	3235	3240
Arg Lys Met Ala Phe Pro Ser Gly Lys Val Glu Gly Cys Met Val	3245	3250	3255
Gln Val Thr Cys Gly Thr Thr Thr Leu Asn Gly Leu Trp Leu Asp	3260	3265	3270
Asp Thr Val Tyr Cys Pro Arg His Val Ile Cys Thr Ala Glu Asp	3275	3280	3285
Met Leu Asn Pro Asn Tyr Glu Asp Leu Leu Ile Arg Lys Ser Asn	3290	3295	3300
His Ser Phe Leu Val Gln Ala Gly Asn Val Gln Leu Arg Val Ile	3305	3310	3315
Gly His Ser Met Gln Asn Cys Leu Leu Arg Leu Lys Val Asp Thr	3320	3325	3330
Ser Asn Pro Lys Thr Pro Lys Tyr Lys Phe Val Arg Ile Gln Pro	3335	3340	3345
Gly Gln Thr Phe Ser Val Leu Ala Cys Tyr Asn Gly Ser Pro Ser	3350	3355	3360
Gly Val Tyr Gln Cys Ala Met Arg Pro Asn His Thr Ile Lys Gly	3365	3370	3375
Ser Phe Leu Asn Gly Ser Cys Gly Ser Val Gly Phe Asn Ile Asp	3380	3385	3390
Tyr Asp Cys Val Ser Phe Cys Tyr Met His His Met Glu Leu Pro	3395	3400	3405
Thr Gly Val His Ala Gly Thr Asp Leu Glu Gly Lys Phe Tyr Gly	3410	3415	3420

Pro	Phe	Val	Asp	Arg	Gln	Thr	Ala	Gln	Ala	Ala	Gly	Thr	Asp	Thr
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Thr	Ile	Thr	Leu	Asn	Val	Leu	Ala	Trp	Leu	Tyr	Ala	Ala	Val	Ile
	3440					3445					3450			
Asn	Gly	Asp	Arg	Trp	Phe	Leu	Asn	Arg	Phe	Thr	Thr	Thr	Leu	Asn
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Asp	Phe	Asn	Leu	Val	Ala	Met	Lys	Tyr	Asn	Tyr	Glu	Pro	Leu	Thr
	3470					3475					3480			
Gln	Asp	His	Val	Asp	Ile	Leu	Gly	Pro	Leu	Ser	Ala	Gln	Thr	Gly
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Asn	Gly	Met	Asn	Gly	Arg	Thr	Ile	Leu	Gly	Ser	Thr	Ile	Leu	Glu
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Asp	Glu	Phe	Thr	Pro	Phe	Asp	Val	Val	Arg	Gln	Cys	Ser	Gly	Val
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Thr	Phe	Gln	Gly	Lys	Phe	Lys	Lys	Ile	Val	Lys	Gly	Thr	His	His
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Trp	Met	Leu	Leu	Thr	Phe	Leu	Thr	Ser	Leu	Leu	Ile	Leu	Val	Gln
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Cys	Thr	Ser	Val	Val	Leu	Leu	Ser	Val	Leu	Gln	Gln	Leu	Arg	Val
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Glu	Ser	Ser	Ser	Lys	Leu	Trp	Ala	Gln	Cys	Val	Gln	Leu	His	Asn
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Asp	Ile	Leu	Leu	Ala	Lys	Asp	Thr	Thr	Glu	Ala	Phe	Glu	Lys	Met
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Val	Ser	Leu	Leu	Ser	Val	Leu	Leu	Ser	Met	Gln	Gly	Ala	Val	Asp
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Tyr	Ala	Thr	Ala	Gln	Glu	Ala	Tyr	Glu	Gln	Ala	Val	Ala	Asn	Gly
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Pro	Lys	Ser	Asp	Gly	Thr	Gly	Thr	Ile	Tyr	Thr	Glu	Leu	Glu	Pro
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Pro	Cys	Arg	Phe	Val	Thr	Asp	Thr	Pro	Lys	Gly	Pro	Lys	Val	Lys
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Phe	Ala	Val	Asp	Pro	Ala	Lys	Ala	Tyr	Lys	Asp	Tyr	Leu	Ala	Ser
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 Gln Ser Ala Asp Ala Ser Thr Phe Leu Asn Gly Phe Ala Val
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 Thr Ser Thr Asp Val Val Tyr Arg Ala Phe Asp Ile Tyr Asn Glu Lys
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 35 40 45
 Glu Lys Asp Glu Glu Gly Asn Tyr Gln His Glu Glu Thr Ile Tyr Asn Leu
 50 55 60
 Arg His Thr Met Ser Asn Tyr Gln His Glu Glu Thr Ile Tyr Asn Leu
 65 70 75 80
 Val Lys Asp Cys Pro Ala Val Ala Val His Asp Phe Phe Lys Phe Arg
 85 90 95
 Val Asp Gly Asp Met Val Pro His Ile Ser Arg Gln Arg Leu Thr Lys
 100 105 110
 Tyr Thr Met Ala Asp Leu Val Tyr Ala Leu Arg His Phe Asp Glu Gly
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 Asn Cys Asp Thr Leu Lys Glu Ile Leu Val Thr Tyr Asn Cys Cys Asp
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 Asp Asp Tyr Phe Asn Lys Lys Asp Trp Tyr Asp Phe Val Glu Asn Pro
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 Asp Ile Leu Arg Val Tyr Ala Asn Leu Gly Glu Arg Val Arg Gln Ser
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 Leu Leu Lys Thr Val Gln Phe Cys Asp Ala Met Arg Asp Ala Gly Ile
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 Val Gly Val Leu Thr Leu Asp Asn Gln Asp Leu Asn Gly Asn Trp Tyr
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 Val Asp Ser Tyr Tyr Ser Leu Leu Met Pro Ile Leu Thr Leu Thr Arg
 225 230 235 240
 Ala Leu Ala Ala Glu Ser His Met Asp Ala Asp Leu Ala Lys Pro Leu
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 Ile Lys Trp Asp Leu Leu Lys Tyr Asp Phe Thr Glu Glu Arg Leu Cys
 260 265 270
 Leu Phe Asp Arg Tyr Phe Lys Tyr Trp Asp Gln Thr Tyr His Pro Asn
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 Cys Ile Asn Cys Leu Asp Asp Arg Cys Ile Leu His Cys Ala Asn Phe
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 Asn Val Leu Phe Ser Thr Val Phe Pro Pro Thr Ser Phe Gly Pro Leu
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 Val Arg Lys Ile Phe Val Asp Gly Val Pro Phe Val Val Ser Thr Gly
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 Tyr His Phe Arg Glu Leu Gly Val Val His Asn Gln Asp Val Asn Leu
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Lys	Gly	Phe	Phe	Lys	Glu	Gly	Ser	Ser	Val	Glu	Leu	Lys	His	Phe	Phe		
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Phe	Ala	Gln	Asp	Gly	Asn	Ala	Ala	Ile	Ser	Asp	Tyr	Asp	Tyr	Tyr	Arg		
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Tyr	Asn	Leu	Pro	Thr	Met	Cys	Asp	Ile	Arg	Gln	Leu	Leu	Phe	Val	Val		
		450										460					
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			485							490				495			
Phe	Asn	Lys	Trp	Gly	Lys	Ala	Arg	Leu	Tyr	Tyr	Asp	Ser	Met	Ser	Tyr		
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Glu	Asp	Gln	Asp	Ala	Leu	Phe	Ala	Tyr	Thr	Lys	Arg	Asn	Val	Ile	Pro		
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Thr	Ile	Thr	Gln	Met	Asn	Leu	Lys	Tyr	Ala	Ile	Ser	Ala	Lys	Asn	Arg		
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Ala	Arg	Thr	Val	Ala	Gly	Val	Ser	Ile	Cys	Ser	Thr	Met	Thr	Asn	Arg		
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Gln	Phe	His	Gln	Lys	Leu	Leu	Lys	Ser	Ile	Ala	Ala	Thr	Arg	Gly	Ala		
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Leu	Lys	Thr	Val	Tyr	Ser	Asp	Val	Glu	Thr	Pro	His	Leu	Met	Gly	Trp		
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Asp	Tyr	Pro	Lys	Cys	Asp	Arg	Ala	Met	Pro	Asn	Met	Leu	Arg	Ile	Met		
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Ala	Ser	Leu	Val	Leu	Ala	Arg	Lys	His	Asn	Thr	Cys	Cys	Asn	Leu	Ser		
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His	Arg	Phe	Tyr	Arg	Leu	Ala	Asn	Glu	Cys	Ala	Gln	Val	Leu	Ser	Glu		
			645							650				655			
Met	Val	Met	Cys	Gly	Gly	Ser	Leu	Tyr	Val	Lys	Pro	Gly	Gly	Thr	Ser		
		660							665				670				
Ser	Gly	Asp	Ala	Thr	Thr	Ala	Tyr	Ala	Asn	Ser	Val	Phe	Asn	Ile	Cys		
		675							680				685				
Gln	Ala	Val	Thr	Ala	Asn	Val	Asn	Ala	Leu	Leu	Ser	Thr	Asp	Gly	Asn		
		690							695				700				
Lys	Ile	Ala	Asp	Lys	Tyr	Val	Arg	Asn	Leu	Gln	His	Arg	Leu	Tyr	Glu		
705							710				715				720		
Cys	Leu	Tyr	Arg	Asn	Arg	Asp	Val	Asp	His	Glu	Phe	Val	Asp	Glu	Phe		
			725							730				735			
Tyr	Ala	Tyr	Leu	Arg	Lys	His	Phe	Ser	Met	Met	Ile	Leu	Ser	Asp	Asp		
		740							745				750				
Ala	Val	Val	Cys	Tyr	Asn	Ser	Asn	Tyr	Ala	Ala	Gln	Gly	Leu	Val	Ala		
		755							760				765				
Ser	Ile	Lys	Asn	Phe	Lys	Ala	Val	Leu	Tyr	Tyr	Gln	Asn	Asn	Val	Phe		
		770							775				780				
Met	Ser	Glu	Ala	Lys	Cys	Trp	Thr	Glu	Thr	Asp	Leu	Thr	Lys	Gly	Pro		
785							790										

Met	Leu	Thr	Asn	Asp	Asn	Thr	Ser	Arg	Tyr	Trp	Glu	Pro	Glu	Phe	Tyr	900	905	910
Glu	Ala	Met	Tyr	Thr	Pro	His	Thr	Val	Leu	Gln	Ala	Val	Gly	Ala	Cys	915	920	925
Val	Leu	Cys	Asn	Ser	Gln	Thr	Ser	Leu	Arg	Cys	Gly	Ala	Cys	Ile	Arg	930	935	940
Arg	Pro	Phe	Leu	Cys	Cys	Lys	Cys	Cys	Tyr	Asp	His	Val	Ile	Ser	Thr	945	950	955
Ser	His	Lys	Leu	Val	Leu	Ser	Val	Asn	Pro	Tyr	Val	Cys	Asn	Ala	Pro	965	970	975
Gly	Cys	Asp	Val	Thr	Asp	Val	Thr	Gln	Leu	Tyr	Leu	Gly	Gly	Met	Ser	980	985	990
Tyr	Tyr	Cys	Lys	Ser	His	Lys	Pro	Pro	Ile	Ser	Phe	Pro	Leu	Cys	Ala	995	1000	1005
Asn	Gly	Gln	Val	Phe	Gly	Leu	Tyr	Lys	Asn	Thr	Cys	Val	Gly	Ser		1010	1015	1020
Asp	Asn	Val	Thr	Asp	Phe	Asn	Ala	Ile	Ala	Thr	Cys	Asp	Trp	Thr		1025	1030	1035
Asn	Ala	Gly	Asp	Tyr	Ile	Leu	Ala	Asn	Thr	Cys	Thr	Glu	Arg	Leu		1040	1045	1050
Lys	Leu	Phe	Ala	Ala	Glu	Thr	Leu	Lys	Ala	Thr	Glu	Glu	Thr	Phe		1055	1060	1065
Lys	Leu	Ser	Tyr	Gly	Ile	Ala	Thr	Val	Arg	Glu	Val	Leu	Ser	Asp		1070	1075	1080
Arg	Glu	Leu	His	Leu	Ser	Trp	Glu	Val	Gly	Lys	Pro	Arg	Pro	Pro		1085	1090	1095
Leu	Asn	Arg	Asn	Tyr	Val	Phe	Thr	Gly	Tyr	Arg	Val	Thr	Lys	Asn		1100	1105	1110
Ser	Lys	Val	Gln	Ile	Gly	Glu	Tyr	Thr	Phe	Glu	Lys	Gly	Asp	Tyr		1115	1120	1125
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Val	Gly	Asp	Tyr	Phe	Val	Leu	Thr	Ser	His	Thr	Val	Met	Pro	Leu		1145	1150	1155
Ser	Ala	Pro	Thr	Leu	Val	Pro	Gln	Glu	His	Tyr	Val	Arg	Ile	Thr		1160	1165	1170
Gly	Leu	Tyr	Pro	Thr	Leu	Asn	Ile	Ser	Asp	Glu	Phe	Ser	Ser	Asn		1175	1180	1185
Val	Ala	Asn	Tyr	Gln	Lys	Val	Gly	Met	Gln	Lys	Tyr	Ser	Thr	Leu		1190	1195	1200
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Ala	Leu	Tyr	Tyr	Pro	Ser	Ala	Arg	Ile	Val	Tyr	Thr	Ala	Cys	Ser		1220	1225	1230
His	Ala	Ala	Val	Asp	Ala	Leu	Cys	Glu	Lys	Ala	Leu	Lys	Tyr	Leu		1235	1240	1245
Pro	Ile	Asp	Lys	Cys	Ser	Arg	Ile	Ile	Pro	Ala	Arg	Ala	Arg	Val		1250	1255	1260
Glu	Cys	Phe	Asp	Lys	Phe	Lys	Val	Asn	Ser	Thr	Leu	Glu	Gln	Tyr		1265	1270	1275
Val	Phe	Cys	Thr	Val	Asn	Ala	Leu	Pro	Glu	Thr	Thr	Ala	Asp	Ile		1280	1285	1290
Val	Val	Phe	Asp	Glu	Ile	Ser	Met	Ala	Thr	Asn	Tyr	Asp	Leu	Ser		1295	1300	1305
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Thr	Leu	Glu	Pro	Glu	Tyr	Phe	Asn	Ser	Val	Cys	Arg	Leu	Met	Lys		1340	1345	1350
Thr	Ile	Gly	Pro	Asp	Met	Phe	Leu	Gly	Thr	Cys	Arg	Arg	Cys	Pro		1355	1360	1365

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Pro	Asn	Met	Phe	Ile	Thr	Arg	Glu	Glu	Ala	Ile	Arg	His	Val	Arg
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<213> Artificial sequence

<220>

<223> SNE-S1 primer

<400> 141

ggttgggatt atccaaaatg tga

23

<210> 142

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> SNE-AS1 primer

<400> 142

gcatcatcag aaagaatcat catg

24

<210> 143

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> SAR1-S primer

<400> 143
 cctctcttgt tcttgctcgc a 21

<210> 144
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> SAR1-AS primer

<400> 144
 tatagtgcgc cgccacacat g 21

<210> 145
 <211> 45
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 145
 ataggatcca ccatgtttat tttcttatta tttcttactc tcact 45

<210> 146
 <211> 37
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 146
 atactcgagt tatgtgtaat gtaatttgac acccttg 37

<210> 147
 <211> 45
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 147
 ataggatcca ccatgtttat tttcttatta tttcttactc tcact 45

<210> 148
 <211> 36
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 148
 acctccggat ttaatatatt gctcatattt tcccaa 36

<210> 149
 <211> 13
 <212> PRT

<213> Artificial sequence

<220>

<223> N-terminal end of SRAS-CoV S protein (amino acids 1 to 13)

<400> 149

Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly
1 5 10

<210> 150

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> oligopeptide

<400> 150

Ser Gly Asp Tyr Lys Asp Asp Asp Asp Lys
1 5 10

<210> 151

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer

<400> 151

actagctagc ggatccacca tggtcatctt cctg

34

<210> 152

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer

<400> 152

agtatccgga cttgatgtac tgctcgtact tgc

33

<210> 153

<211> 59

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotid

<400> 153

tatgagcttt tttttttttt tttttttggc atataaatag actcggcgcg ccatctgca

59

<210> 154

<211> 53

<212> DNA

<213> Artificial sequence

<220>
 <223> oligonucleotid

 <400> 154
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 <210> 155
 <211> 45
 <212> DNA
 <213> Artificial sequence

 <220>
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 <400> 155
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 <210> 156
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 <212> DNA
 <213> Artificial sequence

 <220>
 <223> PCR primer

 <400> 156
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 <210> 157
 <211> 20
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 <400> 157
 ccatttcaac aatttggccg 20

 <210> 158
 <211> 45
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 <220>
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 <400> 158
 ataggatccg cgcgctcatt atttatcgtc gtcattcttta taatc 45